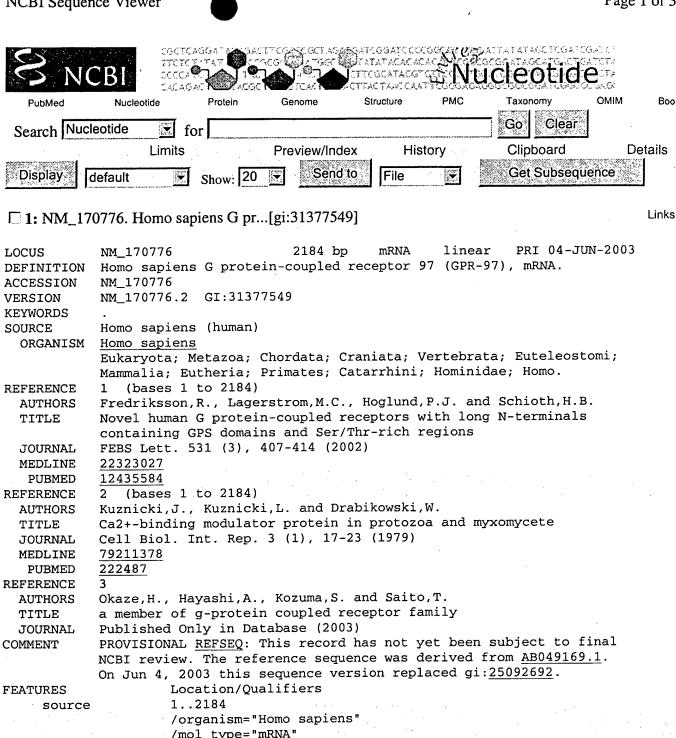
Score = 1122 bits (2870), Expect = 0.0
Identities = 548/549 (99%), Positives = 548/549 (99%)
Frame = +1

Query:	1	MATPRGLGALLLLLLPTSGQEKPTEGPRNTCLGSNNMYDIFNLNDKALCFTKCRQSGSI	
		MATPRGL ALLLLLLPTSGQEKPTEGPRNTCLGSNNMYDIFNLNDKALCFTKCRQSGSI	
Sbjct:	1	MATPRGLWALLLLLLPTSGQEKPTEGPRNTCLGSNNMYDIFNLNDKALCFTKCRQSGSI	180
Query:	61	SCNVENLQRYWLNYEAHLMKEGLTQKVNTPFLKALVQNLSTNTAEDFYFSLEPSQVPRQV	120
		SCNVENLQRYWLNYEAHLMKEGLTQKVNTPFLKALVQNLSTNTAEDFYFSLEPSQVPRQV	•
Sbjct:	181	SCNVENLQRYWLNYEAHLMKEGLTQKVNTPFLKALVQNLSTNTAEDFYFSLEPSQVPRQV	
Query:	121	MKDEDKPPDRVRLPKSLFRSLPGNRSVVRLAVTILDIGPGTLFKGPRLGLGDGSGVLNNR	180
		MKDEDKPPDRVRLPKSLFRSLPGNRSVVRLAVTILDIGPGTLFKGPRLGLGDGSGVLNNR	
Sbjct:	361	MKDEDKPPDRVRLPKSLFRSLPGNRSVVRLAVTILDIGPGTLFKGPRLGLGDGSGVLNNR	
Query:	181	LVGLSVGQMHVTKLAEPLEIVFSHQRPPPNMTLTCVFWDVTKGTTGDWSSEGCSTEVRPE	240
		LVGLSVGQMHVTKLAEPLEIVFSHQRPPPNMTLTCVFWDVTKGTTGDWSSEGCSTEVRPE	
Sbjct:	541	LVGLSVGQMHVTKLAEPLEIVFSHQRPPPNMTLTCVFWDVTKGTTGDWSSEGCSTEVRPE	720
Query:	241	GTVCCCDHLTFFALLLRPTLDQSTVHILTRISQAGCGVSMIFLAFTIILYAFLRLSRERF	300
		GTVCCCDHLTFFALLLRPTLDQSTVHILTRISQAGCGVSMIFLAFTIILYAFLRLSRERF	
Sbjct:	721	${\tt GTVCCCDHLTFFALLLRPTLDQSTVHILTRISQAGCGVSMIFLAFTIILYAFLRLSRERF}$	900
0	201	WORDS BUTTURES COOL FLANTS BY A PROPERCY CONTRACTOR OF THE CONTRAC	1
Query:	301	KSEDAPKIHVALGGSLFLLNLAFLVNVGSGSKGSDAACWARGAVFHYFLLCAFTWMGLEA	360
~1 .		KSEDAPKIHVALGGSLFLLNLAFLVNVGSGSKGSDAACWARGAVFHYFLLCAFTWMGLEA	
Sbjct:	901	${\tt KSEDAPKIHVALGGSLFLLNLAFLVNVGSGSKGSDAACWARGAVFHYFLLCAFTWMGLEA}$	1080
Query:	361	$\verb FHLYLLAVRVFNTYFGHYFLKLSLVGWGLPALMVIGTGSANSYGLYTIRDRENRTSLELC \\$	420
		$\verb FHLYLLAVRVFNTYFGHYFLKLSLVGWGLPALMVIGTGSANSYGLYTIRDRENRTSLELC \\$	
Sbjct:	1081	FHLYLLAVRVFNTYFGHYFLKLSLVGWGLPALMVIGTGSANSYGLYTIRDRENRTSLELC	1260
Query:		WFREGTTMYALYITVHGYFLITFLFGMVVLALVVWKIFTLSRATAVKERGKNRKKVLTLL	480
		WFREGTTMYALYITVHGYFLITFLFGMVVLALVVWKIFTLSRATAVKERGKNRKKVLTLL	
Sbjct:	1261	WFREGTTMYALYITVHGYFLITFLFGMVVLALVVWKIFTLSRATAVKERGKNRKKVLTLL	1440
Query:			540
		GLSSLVGVTWGLAIFTPLGLSTVYIFALFNSLQGVFICCWFTILYLPSQSTTVSSSTARL	
Sbjct:	1441	GLSSLVGVTWGLAIFTPLGLSTVYIFALFNSLQGVFICCWFTILYLPSQSTTVSSSTARL	1620

Query: 541 DQAHSASQE 549 DQAHSASQE Sbjct: 1621DQAHSASQE 1647





/mol_type="mRNA" /db_xref="taxon:9606" /chromosome="16" /map="16q13" 1..2184 gene /gene="GPR-97" /db_xref="LocusID:222487" 47..1696 CDS /gene="GPR-97" /note="EGF-TM7-like" /codon_start=1

/product="G protein-coupled receptor 97" /protein_id="NP_740746.2" /db_xref="GI:31377550" /db_xref="LocusID:222487"



/translation="MATPRGLGALLLLLLLPTSGQEKPTEGPRNTCLGSNNMYDIFNL NDKALCFTKCRQSGSDSCNVENLQRYWLNYEAHLMKEGLTQKVNTPFLKALVQNLSTN TAEDFYFSLEPSQVPRQVMKDEDKPPDRVRLPKSLFRSLPGNRSVVRLAVTILDIGPG TLFKGPRLGLGDGSGVLNNRLVGLSVGQMHVTKLAEPLEIVFSHQRPPPNMTLTCVFW DVTKGTTGDWSSEGCSTEVRPEGTVCCCDHLTFFALLLRPTLDQSTVHILTRISQAGC GVSMIFLAFTIILYAFLRLSRERFKSEDAPKIHVALGGSLFLLNLAFLVNVGSGSKGS DAACWARGAVFHYFLLCAFTWMGLEAFHLYLLAVRVFNTYFGHYFLKLSLVGWGLPAL MVIGTGSANSYGLYTIRDRENRTSLELCWFREGTTMYALYITVHGYFLITFLFGMVVL ALVVWKIFTLSRATAVKERGKNRKKVLTLLGLSSLVGVTWGLAIFTPLGLSTVYIFAL FNSLQGVFICCWFTILYLPSQSTTVSSSTARLDQAHSASQE"

misc_feature

680..814

/gene="GPR-97"

/note="GPS; Region: Latrophilin/CL-1-like GPS domain. Domain present in latrophilin/CL-1, sea urchin REJ and

polycystin"

/db_xref="CDD:pfam01825"

misc_feature

839..1618 /gene="GPR-97"

672 c

/note="7tm_2; Region: 7 transmembrane receptor (Secretin

family)"

413 a

/db_xref="CDD:pfam00002"

597 g

BASE COUNT ORIGIN

> 1 ggccagacag ccacagagct cctggcgtgg gcaaggctgg ccaaggatgg cgacgcccag 121 cgaagggcca agaaacacct gcctggggag caacaacatg tacgacatct tcaacttgaa 181 tgacaagget ttgtgettea ceaagtgeag geagteggge agegaeteet geaatgtgga 241 aaacttgcag agatactggc taaactacga ggcccatctg atgaaggaag gtttgacgca 301 gaaggtgaac acgcctttcc tgaaggcttt ggtccagaac ctcagcacca acactgcaga 361 agaettetat tietetetgg ageeetetea ggiteegagg eaggigatga aggaegagga 421 caageceect gacagagtge gaetteecaa gageettttt egateeetge caggeaacag 481 gtctgtggtc cgcttggccg tcaccattct ggacattggt ccagggactc tcttcaaggg 541 cccccggctc ggcctgggag atggcagcgg cgtgttgaac aatcgcctgg tgggtttgag 601 tgtgggacaa atgcatgtca ccaagctggc tgagcctctg gagatcgtct tctctcacca 661 gcgaccgccc cctaacatga ccctcacctg tgtattctgg gatgtgacta aagggaccac 721 tggagactgg tcttctgagg gctgctccac ggaggtcaga cctgagggga ccgtgtgctg 781 ctgtgaccac ctgacctttt tcgccctgct cctgagaccc accttggacc agtccacggt 841 gcatatecte acacgeatet eccaggeggg etgtggggte tecatgatet teetggeett 901 caccattatt ctttatgcct ttctgaggct ttcccgggag aggttcaagt cagaagatgc 961 cccaaagatc cacgtggccc tgggtggcag cctgttcctc ctgaatctgg ccttcttggt 1021 caatgtgggg agtggctcaa aggggtctga tgctgcctgc tgggcccggg gggctgtctt 1081 ccactacttc ctgctctgtg ccttcacctg gatgggcctt gaagccttcc acctctacct 1141 gctcgctgtc agggtcttca acacctactt cgggcactac ttcctgaagc tgagcctggt 1201 gggctggggc ctgcccgccc tgatggtcat cggcactggg agtgccaaca gctacggcct 1261 ctacaccatc cgtgataggg agaaccgcac ctctctggag ctatgctggt tccgtgaagg 1321 gacaaccatg tacgecetet atateaccgt ceaeggetae tteeteatea cetteetett 1381 tggcatggtg gtcctggccc tggtggtctg gaagatcttc accctgtccc gtgctacagc 1441 ggtcaaggag cgggggaaga accggaagaa ggtgctcacc ctgctgggcc tctcgagcct 1501 ggtgggtgtg acatgggggt tggccatctt caccccgttg ggcctctcca ccgtctacat 1561 ctttgcactt ttcaactcct tgcaaggtgt cttcatctgc tgctggttca ccatccttta 1621 cctcccaagt cagagcacca cagtctcctc ctctactgca agattggacc aggcccactc 1681 cgcatctcaa gaataggaag gcacggccct gcaatatgga ctcagctctg gctctctgtg 1741 tgaccttggg cagctccgtg cctctctctg tactccctca gtttccttct ctgtacaatg 1801 tggctgggga gggagaggat gggaccaggt tggaccacgt ggcatcagag gtcccatcca 1861 gatccaacta taggtccaag agtccacgta agcaggtttg caaggctcta aagttcctat 1921 agtcctgaga ccccctgcca gcaaagagtg acagtcacct ccatgccctg ccctcattgc 1981 aaagccctca ctcaccttct ggtctcagca agggaggaga gtctgttgct ggcatagccc 2041 tggaaggage ecceageete teceeteete eteettgtea etggeeteee acaaeteeee 2101 ttctggctgc ctgtaacctt gaggggcatt caggaggcca gcgttccctc aggcactggg 2161 ggtttgtttt ggggggtggg agtt

//

<u>Disclaimer | Write to the Help Desk</u> <u>NCBI | NLM | NIH</u>

Jul 8 2003 12:22:35